SEO SEARCH SUMMARY

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 06:14:15; Search time 16680 Seconds

(without alignments)

11529.559 Million cell updates/sec

Title:

US-09-753-143-72

Perfect score: 4437

Sequence:

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:

6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb om:*
- 5: gb ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb ro:*
- 11: gb sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em ba:*
- 16: em fun:*
- 17: em hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em ph:*
- 25: em pl:*
- 26: em ro:*
- 27: em_sts:*

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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			8			SUMMA	RIES			Part	ent	
Res	ult		Query							/ .		
	No.	Score		Length	DB	ID			/	Descript	lon	
	1	4437	100.0	4437	6	AR049083	USPN	58245	01/	AR049083	_	
	2	4435.4	100.0	4437	6	AR211947	44	63993	18		Sequence	
	3	4435.4	100.0	4437	6	AX335489					Sequence	
	4	4435.4	100.0	4437	6	AX695780					Sequence	
	5	4435.4	100.0	4437	9	HSU39817	J-Geni	Bank			ıman Bloom	
	6	4252.4	95.8	4254	6	AX695781				AX695781	_	
	7	2925.8	65.9	4498	6	AX695777			_		Sequence	
	8	2925.8	65.9	4498	10	\mathtt{MMBLM}		Ge			us musculi	
	9	2888	65.1	4763	10	AB00867	4				Mus musci	1
	10	2882.6	65.0	4251	6	AX695778				AX695778		
	11	1204.2	27.1	3581	5	AB040747			GB-	AB040747		
	12	1082.8	24.4	4124	5	AF307841					Xenopus 1	
C	13	704	15.9	95565	9	AC000379			GB.		Human Chr	1997
	14	704	15.9	96594	6	AX695779				AX695779		
	15	704	15.9	99500	6	AR211954					Sequence	
	16	704		147854	9	AC021422					Homo sapi	
С	17	704	15.9	157248	9	AC002312				AC002312	Human Chr	
C	18	670.4	15.1	100259	9	AC005800				AC005800	Homo sapi	
	19	670.4	15.1	142201	9	AC124248				AC124248	Homo sapi	
C	20	558.8	12.6	64525	2	AC124238				AC124238	Homo sapi	
	21	534	12.0	630	6	AR211955					Sequence	
	22	460.8	10.4	514	9	BC062697				BC062697	Homo sapi	
C	23	450.6	10.2	198446	2	AC110907				AC110907	Mus muscu	
C	24	441.2	9.9	94175	2	AC136849				AC136849	Rattus no	
	25	425.6	9.6	96593	6	AX695776				AX695776	Sequence	
	26	359.6	8.1	260924	2	AC095740				AC095740	Rattus no	
	27	335.6	7.6	4835	3	DMU92536				U92536 Di	rosophila	
	28	305.4	6.9	3172	3	AY095296				AY095296	Caenorhab	
	29	299.2	6.7	2060	8	ATH40447	0			AJ404470	Arabidops	
	30	269.2	6.1	3567	8	BT010133				BT010133	Arabidops	
	31	269.2	6.1	3891	8	AY120761				AY120761	Arabidops	
	32	269.2	6.1	3916	8	ATH40447	3				Arabidops	
	33	268	6.0	5161	8	SPDNAHEL	G				pombe hus	

OM nucleic - nucleic search, using sw model

July 28, 2004, 06:09:25; Search time 1584 Seconds

(without alignments)

11899.782 Million cell updates/sec

Title: US-09-753-143-72

Perfect score: 4437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues Searched:

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100%

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Listing first 45 summaries

N Geneseq 29Jan04:* Database :

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002s:*

7: geneseqn2003as:*

8: geneseqn2003bs:*

9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length :	DB	ID		Descript	ion
1 2 3 4 5 6 7 8 9 10 11 12 13	4435.4 4435.4 4435.4 4435.4 4435.4 4432.2	100.0 100.0 100.0 100.0 100.0 99.9 99.9	4437 4437 4437 4437 4437 4437 4437 4437	DB 6 6 8 9 9 2 2 2 2 2 2 8	ABL67661 (A) AAD41733 (JS) ADA02889 (A) ADB72627 (A) ADC85368 (A) AAT67013 (A) AAT93390 AAT93390 AAT93395 AAT93394 AAT93391 AAT93389 AAT93389 AAT93389 AAT93389	0 03/057146 0 03/057146 0 03/005853	Abl67661 Aad41733 Ada02889 Adb72627 Adc85368 Aat67013 Aat93390 Aat93395 Aat93395 Aat93391 Aat93389 Aat93389 Aat93389 Aat93393 Ada02890	Oesophagu Human REC Human BLM Human Blm Bloom syn Bloom's s
15 16	4252.4 4252.4	95.8 95.8	4254 4254	9 9	ADB72628 ADC85369			Human BLM Human Blm
17	2925.8	65.9	4498	8	ADA02886		Ada02886	Mouse Blm

OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 00:56:19; Search time 289 Seconds

(without alignments)

8520.128 Million cell updates/sec

Title: US-09-753-143-72

Perfect score: 4437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Resi	ult No.	Score	% Query Match	Length I	DВ	ID	Description
	1	4437	100.0	4437	1	 US-08-559-303B-72	Sequence 72, Appl
	2	4437	100.0	4437	3	US-09-175-828-72	Sequence 72, Appl
	3	4435.4	100.0	4437	4	US-09-798-096-3	Sequence 3, Appli
	4	704	15.9	99500	4	US-09-798-096-10	Sequence 10, Appl
	5	534	12.0	630	4	US-09-798-096-11	Sequence 11, Appl
	6	159.8	3.6	1926	4	US-09-543-681A-187	Sequence 187, App
	7	129	2.9	1830121	4	US-09-557-884-1	Sequence 1, Appli
	8	129	2.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	9	123.6	2.8	1851	4	US-09-107-532A-3604	Sequence 3604, Ap
	10	120.6	2.7	1914	4	US-09-134-001C-2821	Sequence 2821, Ap
C	11	119.2	2.7	2004	4	US-08-956-171E-269	Sequence 269, App
	12	113.6	2.6	1860	4	US-09-489-039A-904	Sequence 904, App

OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 05:30:25; Search time 1843 Seconds

(without alignments)

11804.250 Million cell updates/sec

Title: US-09-753-143-72

Perfect score: 4437

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US06 PUBCOMB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6. / egit2_0/ptodata/2/pabpita/0507_NEW_105.Seq.

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2 6/ptodata/2/pubpna/US09C PUBCOMB.seq:*

12: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2 6/ptodata/2/pubpna/US10C PUBCOMB.seq:*

17: /cgn2 6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

18: /cgn2 6/ptodata/2/pubpna/US60 NEW PUB.seq:*

19: /cgn2 6/ptodata/2/pubpna/US60 PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query No. Score Match Length DB ID Description 4437 9 US-09-753-143-72 Sequence 72, Appl 4437 100.0 Sequence 112, App 4437 9 US-09-962-832-112 2 4435.4 100.0 4435.4 100.0 Sequence 155, App 3 4437 12 US-09-997-722-155 Sequence 420, App 4 4435.4 100.0 4437 13 US-10-342-887-420 Sequence 420, App 4435.4 100.0 4437 13 US-10-172-118-420 4313.4 97.2 4544 16 US-10-062-674-1885 Sequence 1885, Ap 6 7 12 US-09-997-722-156 Sequence 156, App 4252.4 95.8 4254 US-09-997-722-152 Sequence 152, App 2925.8 65.9 4498 12 8 US-09-997-722-153 Sequence 153, App 9 2882.6 65.0 4251 12 704 15.9 96594 12 US-09-997-722-154 Sequence 154, App 10 701 15 US-10-029-386-20899 Sequence 20899, A 11 701 15.8 С Sequence 10217, A 607 9 US-09-867-701-10217 12 581.4 13.1 9.6 96593 12 US-09-997-722-151 Sequence 151, App 13 425.6 Sequence 1166, Ap 509 16 US-10-062-674-1166 14 380 8.6 Sequence 22841, A 15 306 6.9 306 9 US-09-864-761-22841 6.2 2150 13 US-10-425-114-19444 Sequence 19444, A 16 273.4 1584 13 US-10-425-114-3024 Sequence 3024, Ap 254.2 5.7 17 Sequence 3, Appli 250.2 5.6 2925 10 US-09-793-807-3 18 1952 17 US-10-437-963-38862 Sequence 38862, A 5.6 19 246.4 Sequence 28609, A 567 10 US-09-918-995-28609 5.5 20 245.4 Sequence 470, App 2505 13 US-10-425-114-470 21 241 5.4 365 9 US-09-864-761-5348 Sequence 5348, Ap c 22 206.6 4.7 365 9 US-09-864-761-14448 Sequence 14448, A 23 206.6 4.7 Sequence 2, Appli 5868 15 US-10-293-504-2 24 204.6 4.6 Sequence 7199, Ap 558 15 US-10-029-386-7199 25 179.8 4.1 Sequence 1, Appli 6916 15 US-10-293-504-1 26 172 3.9 Sequence 25257, A 1172 13 US-10-282-122A-25257 27 166.2 3.7 Sequence 33030, A 28 161.4 3.6 1800 13 US-10-282-122A-33030 Sequence 12367, A 29 160.6 3.6 2160 13 US-10-282-122A-12367 Sequence 78917, A 30 154.8 3.5 1340 13 US-10-424-599-78917 31 154.4 3.5 1164 13 US-10-424-599-35459 Sequence 35459, A Sequence 40794, A 32 148.2 3.3 1863 13 US-10-282-122A-40794 Sequence 9, Appli 3.2 684707 16 US-10-398-221-9 33 143.8 Sequence 2058, Ap 143.8 3.2 3011208 16 US-10-398-221-2058 34 35 143.2 3.2 1803 13 US-10-282-122A-12144 Sequence 12144, A 142.6 3.2 2481 13 US-10-282-122A-16967 Sequence 16967, A 36 3.2 2127 13 US-10-282-122A-16639 Sequence 16639, A 37 142.4 2145 13 US-10-282-122A-15954 Sequence 15954, A 38 139.6 3.1 1833 13 US-10-282-122A-41841 Sequence 41841, A 39 137.2 3.1 2301 Sequence 29918, A 13 US-10-282-122A-29918 40 137 3.1 Sequence 6988, Ap 3.1 1860 9 US-09-815-242-6988 41 136.6 Sequence 22087, A 1860 13 US-10-282-122A-22087 42 136.6 3.1 Sequence 1, Appli 43 135.4 3.1 2731748 17 US-10-297-465A-1 Sequence 38789, A 44 134.6 3.0 1848 13 US-10-282-122A-38789 45 133 3.0 1830 13 US-10-282-122A-39599 Sequence 39599, A

ALIGNMENTS

OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 09:58:50; Search time 10409 Seconds

(without alignments)

12729.224 Million cell updates/sec

Title: US-09-753-143-72

Perfect score: 4437

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em esthum:*

3: em estin:*

 $4: em_estmu:*$

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em estfun:*

16: em estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:* 24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score March Length DB ID Description	Result			Query				
C 2 947.8 21.4 998.4 4493 11 BC034480 (300 → BC034480 Home Sapi C 2 947.8 21.4 974 9 AL556823 AL556823 AL556823 AL556823 A 810.4 18.3 868 12 BM451903 BM451903 AGENCOURT S 803 18.1 964 12 BG199179 BG199179 RF118458 C 6 781.8 17.6 849 13 BX44542 B43442 BX434442 BX434842 7 776.4 17.5 874 13 BX451969 BX451969 BX451969 B 726.6 16.4 882 12 B1091601 B1091601 602859024 9 711 16.0 772 12 BG772975 BG772975 602721230 10 709.8 16.0 873 13 BX451970 BX451970 BX451970 11 697 15.7 865 13 BQ230262 BQ230262 AGENCOURT 12 695.4 15.7 697 12 B1091772 B1091772 602858823 C 13 683 15.4 784 12 BM041661 BM041661 603614723 14 680.2 15.3 782 14 CF748661 CF748661 UT-M-HJO- 15 679.6 15.3 792 12 BM040993 BM040993 G8144728 C 16 673.4 15.2 688 12 BG875917 BG875917 IL3-CT021 17 669.6 15.1 955 12 BM542461 BM542461 AGENCOURT 19 646 14.6 724 12 BS74669 BS74669 602596672 C 20 642.4 14.5 772 14 CB234345 CB243435 UT-M-FW0- 21 629.4 14.2 801 12 B1655028 B1685028 603310006 22 610.4 13.8 665 10 BE538092 BE538092 601062725 23 609 13.7 648 12 B1655090 BI565900 603294510 24 608 13.7 734 12 B1655090 B165690 603294561 25 607.4 13.7 638 12 B1667071 B1667071 603291250 26 603.6 13.4 201 13 BX643108 BX4419085 BX419085 BX419085 3 596.6 13.4 691 10 BE618504 BE618504 BE618504 G034007.X 3 599.6 13.4 691 10 BE618504 BE618504 BE618504 G034007.X 3 599.6 13.4 691 10 BE618504 BE618504 BE618504 BC618604 G0146294 29 595.6 13.4 691 10 BE618504 BE618504 BE618504 G0146294 29 595.6 13.4 691 10 BE618504 BE618504 BE618504 BC618604 G0146294 29 595.6 13.4 691 10 BE618504 BE618504 BC618604 G0146294 29 595.6 13.4 691 10 BE618504 BE618504 GD797743 CD707743 CD707743 EST24270 28 560.8 13.1 1061 12 BG397477 BG397477 602439306 30 584.4 13.2 610 13 BX643048 BX64	Res		Saore		Lenath	חB	TD	Description
C 2 947.8 21.4 974 9 AL556823 AL556823 AL556823 AL55683 AL55683 AL55683 AL55683 AL55683 AL55683 AL55683 AL55683 AL55683 AL556833 AL556853 AL556853 AL556853 AL556853 AL556853 AL556853 AL55683 AL556853 A		NO.	30016	PIACCII I				
C 2 947.8 21.4 974 9 AL556823 AL556823 AL556823 AL55683 AL5568363 AL55683 AL55683 AL55683 AL55683 AL5568363 AL55683 AL556853 AL556853 AL556853 AL556853 AL556853 AL556853 AL556853 AL556853 AL55683 AL556853 AL568533 AL556853 AL56853	-	1	4364.2	98.4	4493	11	BC034480(2007)) BC034480 Homo sapi
1	С						AL556823	AL556823 AL556823
4 810.4 18.3 868 12 BM451903 BM451903 BG199179 BG199179 BG199179 RG199179 RG79975 RG766 RG4 RG2 RG210601 BI091601 G02859024 RG779975 RG772975 RG77297	•					9	AL556853	AL556853 AL556853
5 803 18.1 964 12 BG199179 BG199179 BG199179 BST18458 C 6 781.8 17.6 849 13 BX434842 BX434842 BX434842 BX434842 BX434842 BX451969 BX451969 BX451969 BX451969 BX451969 BX451969 BX451969 BX451969 BX451969 BX451970 BT072975 G02701230 10 709.8 16.0 873 13 BX451970								BM451903 AGENCOURT
C 6 781.8 17.6 849 13 BX434842 BX451969 BX451970 BX651970 BX651970 BX651970 BX651970 BX651970 BX651970 BX451970 B								BG199179 RST18458
7 776.4 17.5 874 13 BX451969 BX451969 BX451969 BY 8 726.6 16.4 882 12 B1091601 B1091601 602859024 9 711 16.0 772 12 BG9772975 BG772975 602721230 10 709.8 16.0 873 13 BX451970	С							BX434842 BX434842
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9 711 16.0 772 12 BG772975 BG772975 602721230 10 709.8 16.0 873 13 BX451970 BX451970 BX451970 11 697 15.7 865 13 BQ230262 BQ230262 AGENCOURT 12 695.4 15.7 697 12 BI091772 BI091772 602858B23 C 13 683 15.4 784 12 BM041661 BM041661 603614723 14 680.2 15.3 782 14 CF748661 CF748661 UI-M-HJU- 15 679.6 15.3 792 12 BM040993 BM040993 603614723 C 16 673.4 15.2 688 12 BG875917 BG875917 II3-CT021 17 669.6 15.1 955 12 BM542461 BM542461 AGENCOURT 18 659.4 14.9 774 14 CA317178 CA317178 UI-M-FW0- 19 646 14.6 724 12 BG574669 BG574669 602596672 C 20 642.4 14.5 772 14 CB243435 CB243435 UI-CF-FN0- 21 629.4 14.2 801 12 BI685028 BI685028 BI685028 603310006 22 610.4 13.8 665 10 BE538092 BE538092 601062725 23 609 13.7 648 12 BG721596 BG721596 602695720 24 608 13.7 734 12 BI656900 BI656900 603284510 25 607.4 13.7 638 12 BI667071 BI667071 603291250 26 603.6 13.6 861 12 BI685164 BI691674 603307363 27 596.8 13.5 664 14 CD707743 CD707743 EST24270 28 596.6 13.4 691 10 BE618504 BE618504 601462944 29 595.6 13.4 691 10 BE618504 BE618504 601462944 29 595.6 13.4 120 13 BX419085 BX419085 BX419085 BX419085 30 584.4 13.2 610 13 BX643048 BX643048 DKFZp781H 35 567.2 12.8 825 14 CF411420 CD707743 EST24270 34 588 13.1 1061 12 BG397477 BG397477 G02439306 35 590.8 13.1 960 12 BG397477 BG397477 G02439306 36 564.8 12.7 575 10 AW502890 AW502890 UI-HF-BN0 37 559.6 12.6 1090 12 BM804157 BM804157 AGENCOURT 38 558 12.6 610 13 BX475196 BK375196 DKFZp6861 39 547.4 12.3 693 10 BE5389560 BE538956 061512475 40 534 12.0 630 9 AI114820 AH1429 Hu 43 516.8 11.6 523 13 BX106802 BA160802 AL120858 DKFZp762J								BI091601 602859024
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43 516.8 11.6 523 13 BX106802		41	535.2	12.1	977	10	BE889560	
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	С	45	514.2	11.6	747	10	BE963549	BE963549 601657344